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208010*E2E4E660

Human 33410

Carboxylesterase Domain

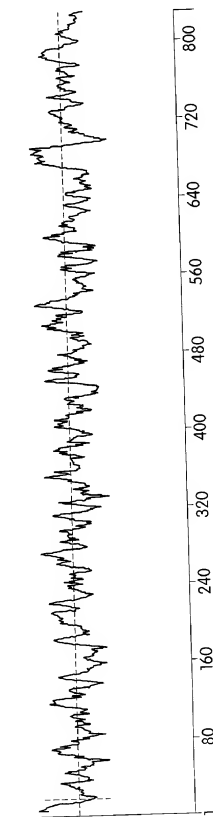


Fig. 1

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COesterase: domain 1 of 1, from 42 to 601: score 440.0, E = 2.1e-128
 *->llVatnnVlcGkvrGvnekttdn...geqsvysr1GIPYAePPVGNlR
 +V+T + G vrGv++ ++n+ g +v Flg+PYA PP+G R
 Fbh33410FL 42 PVVNTAY---GRVGRVRELNNeilG--PVVQFLGVFPYATPPLGARR 83

FkaPqPYkepWsdvldAtkyppsClQdddfgfsldLKva.lkmlslgwn
 F +P+ + W +v+++At+ pp+C+Q+ g +++ +ml+ ++
 Fbh33410FL 84 FQPPEA-PASWPQVGRNATLTPPACPQNLH-G-----ALpAImLVWFT 124

klvg.....lklsEDCLYLNvYtPkntkpn.....
 ++ + +sEDCLYLN y+P + p +++++ +++++ ++
 Fbh33410FL 125 DNLaaatyvQNQSEDCLYLNLYVPTEDGPLTkkrdeatlnppdtdirdp 174

.klFVmVwIhGGGFmfGgshslplslYdgeslaregnVivVsiNYRLGpl
 +k Pvm + hGg +m G+g + dg+ la+ gnViv ++NYRLG+1
 Fbh33410FL 175 gKKPVMLFLHGGSYMEGTG-----NMFDGSVLAAYGNVIVATNLNYRLGLV 219

GFLstgddklpgsGnyGLlDQrlAlKwVqdNiaaFGGDPnsVTifGeSAG
 GFLstgd + GnyGLlDQ+ AL+W +Nia+FGGDP+++TifG AG
 Fbh33410FL 220 GFLSTGDQAAK--GNYGLLDQIQALRWLSENIAHFGGDFERITIFGSGAG 267

aaSVsl1lllsngGDNppsskgLFhRAIsqSGsalspwaigsesnargrak
 a+ V 1l+ls +s+gLF++AI qSG+a+s w++ + ++
 Fbh33410FL 268 ASCVNL1LILS-----HHSEGLFQKAIAQSGTAISSSWSVNYQP--LKYTR 309

elarllGcnetsssellldCLRksaeleleatrslfillfeyvpflplflaf
 la+++GC+++++s+ ++CLR+k+++eL++ +++++Y + +
 Fbh33410FL 310 LLAAKVGCdREDSAEAVECLRRKPSRELVDQDV--QPARYHIAFG----- 352

gPvVDGdDapeafipedPeelikeGkfadvPyliGvtkdEGgyfaamln
 PvvDGD ++p+dPe+l +G f + ++liGv++ EG+ f +
 Fbh33410FL 353 -PVVDGD-----VVPDDPEILMQGEFLNYDMLIGVNGEGLKFV---E 392

asskgedelkktnpdvwllellkyllfyasealnikdMddladkvlekYp
 +s+ +ed ++ ++ + ++ l++ +e + d l +++ Y+
 Fbh33410FL 393 DSAESEDGVSASAFDF-TVSNFVDNLYGYPEGK-----DVLRETIKFMYT 436

gdvddfsvesrkpnlgdmltDlIFkcptrvaadlhakhggsPvYaYvfdh
 +++d+ e r++ l+ ++tD+ + p +va ++ ++ +sPvY+Y f h
 Fbh33410FL 437 DWADRDNGEMRRKTLALFTDHQWVAP-AVATAKLHADYQSPVYFTFTFYH 485

pasfgigQflakrvdpfegggavHgdEiffvFgnpllkqglyka...tee
 + + +pe+ a HgdE+++vFg+p + + + + + + +
 Fbh33410FL 486 HCQ-----AEGRFEWADAAGDELFPYVFGVPMVGATDLFPcnfSKND 527

eksssktmnywanFaktGnFn....ngts.....nglvvWpkytse
 +++s ++m yw+nFaktG+Fn++ + +t +++++++vW k++s+
 Fbh33410FL 528 VMLS-AVVMTYTWNFAKTGDPNGqvpQDTKfihtkpnrFEEVWNSKFNSK 576

eqkYsl1llilttitaqklkardprkvlcnfw<+*
 e +l+l l+ +++++a++ ++fw
 Fbh33410FL 577 EKQ-YLHIGLKPRVRDNYRANK-----VAFW 601

Fig. 2

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CLUSTAL W (1.74) multiple sequence alignment

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Fbh33410FL MWLLALCLVLGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFFVFNATYGRVRGVRRRLNN
ratNL2 = MWLLALCLVLGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFFVFNATYGRVRGVRRRLNN
*****

Fbh33410FL EILGPVVQFLGVPYATPPLGARRFQPEAPASWPGVRNATTLPPACPNLHGALPAIMLP
ratNL2 EILGPVVQFLGVPYATPPLGARRFQPEAPASWPGVRNATTLPPACPNLHGALPAIMLP
*****

Fbh33410FL VWFDTNLEAAATYVQNQSEDCLYLNLVYPTEDGPLTKKRDEATLNPPDPTDIRDPGKKFVM
ratNL2 VWFDTNLEAAATYVQNQSEDCLYLNLVYPTEDGPLTKKRDEATLNPPDPTDIRDPGKKFVM
*****

Fbh33410FL LFLHGGSYMEGTGNMFDGSLAAYGNVIVATLNLYRLGVLGFLSTGDQAAGNYGLLDIQ
ratNL2 LFLHGGSYMEGTGNMFDGSLAAYGNVIVATLNLYRLGVLGFLSTGDQAAGNYGLLDIQ
*****

Fbh33410FL ALRWLSENIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIASGTAISSWSV
ratNL2 ALRWLSENIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIASGTAISSWSV
*****

Fbh33410FL NYQPLKYTRLAALKVCGDREDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDV
ratNL2 NYQPLKYTRLAALKVCGDREDSAEAVECLRRKPSRELVDQVQPARYHIAFGPVVDGDV
*****

Fbh33410FL PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESDGVSAFADFTVSNFVDNLVGY
ratNL2 PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESDGVSAFADFTVSNFVDNLVGY
*****

Fbh33410FL PEGKDVLRITIKFMYTDWADRNGEMRRKTLALFTDHQWVAPAVATAKLHADYQSPVYF
ratNL2 PEGKDVLRITIKFMYTDWADRNGEMRRKTLALFTDHQWVAPAVATAKLHADYQSPVYF
*****

Fbh33410FL YTFYHHCQAEGRPEWADAAGDELPLYVFGVFMVGATDLFFPCNFNSKNDVMSAVVMTYTNT
ratNL2 YTFYHHCQAEGRPEWADAAGDELPLYVFGVFMVGATDLFFPCNFNSKNDVMSAVVMTYTNT
*****

Fbh33410FL FAKTGDPNQVPVQDTKFIHTKPNRPEEVVWSKFNSEKQYLHIGLKPRVRDNRANKVAF
ratNL2 FAKTGDPNQVPVQDTKFIHTKPNRPEEVVWSKFNSEKQYLHIGLKPRVRDNRANKVAF
*****

Fbh33410FL WLELVPHLHNLHTELFTTTTLRPPYATRWPPRP-AGAPGTRRPPPPATLPPEPEPEPGP
ratNL2 WLELVPHLHNLHTELFTTTTLRPPYATRWPPRP-AGAPGTRRPPPPATLPPEPEPEPGP
*****

Fbh33410FL TM1
ratNL2 RAYDRPGDSRDYSTELSVTVAVGASLLFLNLIFAALYKYRDRRQELRCRRLSPPGGSG
RAYDRPGDSRDYSTELSVTVAVGASLLFLNLIFAALYKYRDRRQELRCRRLSPPGGSG
*****

Fbh33410FL SGVPGGGPLLPAAGRELPPPEELVSLQLKRGGVGADPAEALRPACPDYTLALRRAPDD
ratNL2 SGVPGGGPLLPAAGRELPPPEELVSLQLKRGGVGADPAEALRPACPDYTLALRRAPDD
*****

Fbh33410FL VPLLAPGALTLPLSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV
ratNL2 VPLLAPGALTLPLSGLGPPPPPPPSLHPFGPPPPPPPTATSHNNTLPHPHSTTRV
*****

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Fig. 3

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CLUSTAL W (1.74) multiple sequence alignment

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Fbh33410FL MWLLALCLVLGLAGAQRRGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVGRVRELN
KIAA1366 -----

Fbh33410FL EILGPVVQFLGVYATPPLGARFQPEAPASWPGVNRATLPPACPQNLHGALPAIMLP
KIAA1366 -----

Fbh33410FL VWFTDNLEAAATYVQNQSEDCLYLNLVPTEDGPLTKKRDEATLNPPDITDIRDPGKKPVM
KIAA1366 -----

Fbh33410FL LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNRYLGVLFGLSTGDQAAGNYGLLDQIQ
KIAA1366 -----

Fbh33410FL ALRWLSENIAHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIASGTAISSWSV
KIAA1366 -----KAIASGTAISSWSV
*****

Fbh33410FL NYQPLKYTRLAAKVGCDREDSAAEAVECLRRKPSRELVDQDVQPARVHIAFGFVVDGDVV
KIAA1366 NYQPLKYTRLAAKVGCDREDSAAEAVECLRRKPSRELVDQDVQPARVHIAFGFVVDGDVV
*****

Fbh33410FL PDDPEILMQQGEFLNYDMLIGVNGQEGKLFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
KIAA1366 PDDPEILMQQGEFLNYDMLIGVNGQEGKLFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
*****

Fbh33410FL PEGKDVLRETIKFMYTDWADRNGEMRRKTLTLLFTDQHWVAPAVATAKLHADYQSPVYF
KIAA1366 PEGKDVLRETIKFMYTDWADRNGEMRRKTLTLLFTDQHWVAPAVATAKLHADYQSPVYF
*****

Fbh33410FL YTFYHHCQAEGRPEWADAAGDELPIYVFGVPMVGATDLFPCNFSKNDVMLS AVVMTYTWN
KIAA1366 YTFYHHCQAEGRPEWADAAGDELPIYVFGVPMVGATDLFPCNFSKNDVMLS AVVMTYTWN
*****

Fbh33410FL FAKTGDPNQVPVQDTKFIHTKPNRFEEVVSFKFSKEKQYLHIGLKPRVRDNYRANKVAF
KIAA1366 FAKTGDPNQVPVQDTKFIHTKPNRFEEVVSFKFSKEKQYLHIGLKPRVRDNYRANKVAF
*****

Fbh33410FL WLELVPHLNLHTELFTTTTTLRPPYATRWPPRPAGAPGTRPPPPATLPPEPEPEPGPR
KIAA1366 WLELVPHLNLHTELFTTTTTLRPPYATRWPPRPAGAPGTRPPPPATLPPEPEPEPGPR
*****

Fbh33410FL AYDRFPGDSRDYSTELSVTVAVGASLLFLNLLFAALYYKRRDRQELRCRRLSPPGSGS
KIAA1366 AYDRFPGDSRDYSTELSVTVAVGASLLFLNLLFAALYYKRRDRQELRCRRLSPPGSGS
*****

Fbh33410FL GVPGGGFLPAAGRELPEEELVSLQLKRGCGVGADPAEALRPACPDYTLALRRAPDDV
KIAA1366 GVPGGGFLPAAGRELPEEELVSLQLKRGCGVGADPAEALRPACPDYTLALRRAPDDV
*****

Fbh33410FL PLLAPGALTLLPSGLGPPPPPPPSLHFGFPFPPPPPTATSHNNTLPHPHSTTRV
KIAA1366 PLLAPGALTLLPSGLGPPPPPPPSLHFGFPFPPPPPTATSHNNTLPHPHSTTRV
*****
  
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Fig. 4

0934323.010802